



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 157552

TO: Nita M Minnifield
Location: rem/3C01/3C18
Art Unit: 1645
Thursday, June 30, 2005

Case Serial Number: 09/196161

From: Noble Jarrell
Location: Biotech-Chem Library
Rem 1B71
Phone: 272-2556

Noble.jarrell@uspto.gov

Search Notes

*Reviewed
7-1-05
M*

STIC-Biotech/ChemLib

157552

me

From: Chan, Christina
Sent: Monday, June 27, 2005 10:14 AM
To: Minnifield, Nita; STIC-Biotech/ChemLib
Subject: RE: rush sequence search

Please ~~rush~~. Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

RECEIVED
JUN 27 2005
(STIC)

-----Original Message-----

From: Minnifield, Nita
Sent: Sunday, June 26, 2005 10:00 AM
To: Chan, Christina
Subject: rush sequence search

Christina,
Please approve, 2 month amdt. due.
Thanks,
Minnifield

STIC

09/196161

Please do a commercial and interference sequence search on SEQ ID NO: 1 of this application.

Please search both aa and nt databases.

Please provide a paper copy of the results.

Thanks,
Minnifield,
71976
Art Unit 1645
Office REM-3C01
Mailbox REM-3C18

STAFF USE ONLY

Searcher: Noble
Searcher Phone: 2-
Date Searcher Picked up: 6/30/05
Date Completed: 5
Searcher Prep/Rev. Time: 5
Online Time: 5

Type of Search

NA#: 1 AA#: 1
Interference: ✓ SPDI:
S/L: Oligomer:
Encode/Transl:
Structure#: Text:
Inventor: Litigation:

Vendors and cost where applicable

STN:
DIALOG:
QUESTEL/ORBIS:
LEXIS/NEXIS:
SEQUENCE SYSTEM: Cambridge
WWW/Internet:
Other(Specify):

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 30, 2005, 05:17:22 ; Search time 2572 Seconds

(without alignments)
256.057 Million cell updates/sec

Title: US-09-196-161D-1

Sequence: 1 GAAAGGANGGPPANNAAR.....PGGAPGVYFAGAAAGV 105

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 631374 segs, 3136092125 residues

Total number of hits satisfying chosen parameters: 12626748

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame_plus_p2n.model -DEV=xlh
-G=/cgn2_1/USPTO.spool.h/US09196161/runat_28062005_090809_20882/app_query.fasta_1.263
-DB=Published Applications NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPEL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum62
-TRANS=human40.cdi -LIST=45 -LOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09196161 @CGN_1_1460 @runat_28062005_090809_20882
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-YGAPOP=6 -YGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA:
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:
16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:
17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:
18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:
19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq:
20: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:
21: /cgn2_6/ptodata/2/pubpna/US10J_PUBCOMB.seq:
22: /cgn2_6/ptodata/2/pubpna/US10K_PUBCOMB.seq:
23: /cgn2_6/ptodata/2/pubpna/US10L_PUBCOMB.seq:
24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:
25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:
26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	495	88.7	1326	21	US-10-878-694-7
2	495	88.7	2811	21	US-10-878-694-3
3	495	88.7	2811	21	US-10-878-694-4
4	212	38.0	1404	21	US-10-878-694-8
5	84.5	15.1	4355	18	US-10-263-929-95
6	84.5	15.1	5216	18	US-10-263-929-93
7	84.5	15.1	6056	18	US-10-466-720-21
8	84.5	15.1	7244	17	US-10-120-988-143
9	84.5	15.1	8589	17	US-10-085-198-15
10	84	15.1	2335	9	US-09-996-620-9
11	84	15.1	2359	9	US-09-996-620-17
12	83	14.9	3989	15	US-10-053-662A-1
13	82	14.7	669	16	US-10-424-599-139576
14	80.5	14.4	783	17	US-10-282-122A-13344
15	80.5	14.4	1834	18	US-10-425-114-32066
16	80.5	14.4	2023	20	US-10-425-115-54885
17	80	14.3	624	13	US-10-027-632-220391
18	80	14.3	624	17	US-10-027-632-220391
19	80	14.3	6425	19	US-10-322-281-350
20	79	14.2	969	19	US-10-437-963-50968
21	79	14.2	2388	13	US-10-029-180-51
22	79	14.2	2388	21	US-10-952-045-51
23	79	14.2	8077	21	US-10-764-420-2784
24	78	14.0	11009	9	US-09-845-583-1
25	78	14.0	11009	14	US-10-037-182-3
26	78	14.0	11009	21	US-10-764-420-947
27	78	14.0	9025608	15	US-10-156-761-1
28	77.5	13.9	929	20	US-10-653-047-7620
29	77.5	13.9	1213	9	US-09-921-823-1
30	77.5	13.9	1722	18	US-10-389-647-247
31	77.5	13.8	1328	21	US-10-825-692-17
32	77	13.8	3657	19	US-10-437-963-26197
33	77	13.8	6130	9	US-09-970-318-3
34	77	13.8	11558	10	US-09-949-029-133
35	76.5	13.7	3057	18	US-10-263-929-94
36	76	13.6	5113	17	US-10-603-725-11
37	76	13.6	5264	17	US-10-603-725-9
38	76	13.6	6442	19	US-10-437-963-16526
39	75.5	13.5	386	18	US-10-424-599-130425
40	75.5	13.5	646	21	US-10-487-901-1775
41	75.5	13.5	646	21	US-10-487-901-4220
42	75.5	13.5	701	13	US-10-027-632-125233
43	75.5	13.5	701	17	US-10-027-632-125233
44	75.5	13.5	519599	22	US-10-737-082-73
45	75.5	13.5	519599	22	US-10-765-790-73

ALIGNMENTS

RESULT 1
US-10-878-694-7
Sequence 7, Application US/10878694
Publication No. US20050106164A1
GENERAL INFORMATION:
APPLICANT: GARRIG, Jacek
APPLICANT: DICKERSON Jr., Harry W.
APPLICANT: CLARK, Theodore G.
TITLE OF INVENTION: THE UNIVERSITY OF GEORGIA RESEARCH FOUNDATION, INC
TITLE OF INVENTION: RECOMBINANT EXPRESSION OF HETEROLOGOUS NUCLEIC ACIDS IN
FILE REFERENCE: 235, 00100101
CURRENT APPLICATION NUMBER: US/10/878,694
PRIOR FILING DATE: 2004-06-28
PRIOR APPLICATION NUMBER: US/09/498,612
PRIOR FILING DATE: 2000-02-04

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 30, 2005, 04:01:43 / Search time 155 Seconds
(without alignments)
1108.446 Million cell updates/sec

Title: US-09-196-161D-1
Perfect score: 558
Sequence: 1 GAAOGEANGNCPFAANNAR.....POGEAPGVVPAAGAAAGV 105

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1202784 segs, 81818359 residues
Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODE=frame_p2n.model -DEV=x1h
-O=/cgn2_1/USPTO_spool_h/US09196161/rnucat_28062005_090807_20808/app_query.fasta_1.263
-DB=Issued Patents NA -QFMT=fastap -SUFFIX=rm1 -MINMATCH=0.1 -LOOPEXT=0
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -COMPRMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USBR=US09196161 -CGN1_1.69 -rnatcat_28062005_090807_20808 -NCPD=6 -ICPU=3
-NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -OSBLOCK=100 -LONGLOC
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- 1: Issued Patents NA:*
- 2: /cgn2_6/prodata/1/ina/5A.COMB.seq:*
- 3: /cgn2_6/prodata/1/ina/5B.COMB.seq:*
- 4: /cgn2_6/prodata/1/ina/5A.COMB.seq:*
- 5: /cgn2_6/prodata/1/ina/5B.COMB.seq:*
- 6: /cgn2_6/prodata/1/ina/BACKILL1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	84.5	15.1	7244	4	US-09-774-528-143
2	84	15.1	2335	3	US-09-026-001A-9
3	84	15.1	2335	3	US-09-026-001A-17
4	79	14.2	2388	4	US-10-029-180-51
5	78	14.0	11009	4	US-09-845-583A-1
6	77.5	13.9	996	4	US-09-252-991A-11818
7	77.5	13.9	1545	4	US-09-252-991A-11865
8	77.5	13.9	2589	4	US-09-252-991A-11884
9	77.5	13.9	11220	4	US-09-949-016-5061
10	77	13.8	1320	4	US-08-419-414-1
11	77	13.8	6330	4	US-09-949-016-914
12	76	13.6	5113	4	US-09-560-385A-11

13	76	13.6	5264	4	US-09-560-385A-9	Sequence 9, Appl1
14	75	13.4	3620	4	US-09-560-385A-31	Sequence 31, Appl1
15	75	13.4	3720	4	US-09-560-385A-29	Sequence 29, Appl1
16	75	13.4	4316	1	US-08-317-450B-14	Sequence 14, Appl1
17	75	13.4	4316	3	US-08-800-593-14	Sequence 14, Appl1
18	75	13.4	5020	4	US-09-560-385A-27	Sequence 27, Appl1
19	75	13.4	5156	3	US-09-643-597-130	Sequence 130, App
20	75	13.4	5156	4	US-09-480-884A-130	Sequence 130, App
21	75	13.4	5156	4	US-09-542-615A-130	Sequence 130, App
22	75	13.4	5156	4	US-09-606-421B-130	Sequence 130, App
23	75	13.4	5156	4	US-09-221-107-130	Sequence 130, App
24	75	13.4	5156	4	US-09-466-396A-130	Sequence 130, App
25	75	13.4	5156	4	US-09-476-496A-130	Sequence 130, App
26	75	13.4	5156	4	US-09-630-940B-130	Sequence 130, App
27	75	13.4	5156	4	US-09-285-479-130	Sequence 130, App
28	75	13.4	5200	1	US-08-317-450B-12	Sequence 12, Appl1
29	75	13.4	5200	3	US-08-800-593-12	Sequence 12, Appl1
30	75	13.4	5200	4	US-09-560-385A-25	Sequence 25, Appl1
31	74	13.3	28055	4	US-09-949-016-1441	Sequence 1441, A
32	73.5	13.2	468	3	US-08-600-982-29	Sequence 29, Appl1
33	73.5	13.2	468	5	PCT-US94-10261A-29	Sequence 29, Appl1
34	73.5	13.2	846	4	US-09-902-540-8701	Sequence 8701, Ap
35	73.5	13.2	915	4	US-09-489-039A-4735	Sequence 4735, Ap
36	73.5	13.2	5170	4	US-09-560-385A-3	Sequence 3, Appl1
37	73.5	13.2	5280	4	US-09-560-385A-1	Sequence 1, Appl1
38	73.5	13.2	5373	4	US-09-560-385A-7	Sequence 7, Appl1
39	73.5	13.2	5433	4	US-09-560-385A-5	Sequence 5, Appl1
40	73.5	13.2	5496	3	US-08-600-982-23	Sequence 23, Appl1
41	73.5	13.2	5496	5	PCT-US94-10261A-23	Sequence 23, Appl1
42	73.5	13.2	7109	4	US-09-902-540-922	Sequence 922, App
43	73	13.1	2310	4	US-09-489-039A-5030	Sequence 5030, Ap
44	73	13.1	4403765	3	US-09-103-840A-2	Sequence 2, Appl1
45	73	13.1	4411529	3	US-09-103-840A-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-09-774-528-143
Sequence 143, Application US/09774528
Patent No. 6743619
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Zhou, Ping
APPLICANT: Goodrich, Ryle
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Ren, Feiyang
APPLICANT: Zhang, Jie
APPLICANT: Zhao, Qing A.
APPLICANT: Yang, Yonghong
APPLICANT: Xue, Aldong J.
APPLICANT: Wehrman, Tom
APPLICANT: Wang, Jian-Rui
APPLICANT: Wang, Dunrui
APPLICANT: Dimenac, Radoje T.
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 802
CURRENT APPLICATION NUMBER: US/09/774,528
CURRENT FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 441
SOFTWARE: pc_fl_genes Version 2.0
SEQ ID NO 143
LENGTH: 7244
TYPE: DNA
ORGANISM: Homo sapiens
FEATURES:
NAME/KEY: CDS
LOCATION: (714)..(6518)
US-09-774-528-143
Alignment Scores:

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_pjn model

Run on: June 30, 2005, 03:55:12 ; Search time 3372 Seconds
(without alignments)
1508.837 Million cell updates/sec

Title: US-09-196-161D-1

Perfect score: 558
Sequence: 1 GAAQGANQNPFAANNAAR.....PQGAPEGVYFAAGAAAGV 105

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame+pn.model -DEV=xlh
-Q/cgml_1/USPTO.spool_h/US9191611/runat.28062005.090806.20783/app.query.fasta_1.263
-DB=GenBml -QFMT=faastap -SUFFIX=rge -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blomsu62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pcr -NOR=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USER=US9191611@CGML_1.1.3731@runat.28062005.090806.20783 -NCFU=6 -ICPU=3
-NO_MMAP -LARGEOQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -MARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenBml:.*
1: gb_ba:.*
2: gb_hgt:.*
3: gb_in:.*
4: gb_cm:.*
5: gb_ov:.*
6: gb_pat:.*
7: gb_ph:.*
8: gb_pl:.*
9: gb_dr:.*
10: gb_ro:.*
11: gb_sts:.*
12: gb_sy:.*
13: gb_un:.*
14: gb_vl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	495	88.7	1249	3	ICYMANT
2	495	88.7	2486	3	AF140273 Ichthyoph
3	212	38.0	3026	3	AF344424 Ichthyoph
4	194	34.8	1520	3	AF405431 Ichthyoph

Result No.	Score	Query Match	Length DB	ID	Description
5	93	16.7	1644	3	AF298862
6	93	16.7	2066	3	GIASOAB
7	92.5	16.6	133860	3	AF157709
8	91.5	16.4	1163	3	AF312775
9	88.5	15.9	921	6	CO587859
10	88.5	15.9	1041	3	AY061512
11	87.5	15.7	186858	9	AL356585
12	85.5	15.3	60090	9	U30252
13	85	15.2	2730	3	AY142126
14	85	15.2	37443	9	AC144831
15	85	15.2	188644	9	AC090518
16	85	15.2	198489	2	AC067809
17	85	15.2	209706	2	AC067885
18	84.5	15.1	5295	10	BC060277
19	84.5	15.1	5528	10	AK122377
20	84.5	15.1	5693	10	BC036727
21	84.5	15.1	6056	6	AX592784
22	84.5	15.1	6228	9	AB011541
23	84.5	15.1	7244	6	AR541895
24	84.5	15.1	8307	9	AY280362
25	84.5	15.1	8589	6	AX921022
26	84.5	15.1	9921	6	BD185469
27	84	15.1	917	3	AF312772
28	84	15.1	1084	3	AF312771
29	84	15.1	1102	3	AF312770
30	84	15.1	1639	11	BV177181
31	83.5	15.0	174928	10	AC121975
32	83	14.9	3475	3	AF235028
33	83	14.9	3991	4	AY082802
34	82.5	14.8	196620	2	AC145502
35	82.5	14.8	233738	2	AC145502
36	82.5	14.6	2965	9	BC012775
37	81.5	14.6	2965	9	AF099799
38	81.5	14.6	67849	2	AC134685
39	81.5	14.6	110000	1	BX571965
40	81.5	14.6	145247	9	AF186192
41	81	14.5	5943	3	AF354542
42	81	14.5	5943	5	AF468050
43	81	14.5	13867	1	AB011726
44	81	14.5	247196	2	AC073822
45	80.5	14.4	2549	3	AF202776

ALIGNMENTS

Result No.	Score	Query Match	Length DB	ID	Description
1	495	88.7	1249	3	ICYMANT
2	495	88.7	2486	3	AF140273 Ichthyoph
3	212	38.0	3026	3	AF344424 Ichthyoph
4	194	34.8	1520	3	AF405431 Ichthyoph

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 30, 2005, 03:58:39 ; Search time:2653 Seconds
(without alignments)
1506.501 Million cell updates/sec

Title: US-09-196-161D-1
Perfect score: 558
Sequence: 1 GAAQGEANGNQPPAANNAAR.....POGEAPGVGVFAAGAAAGV 105

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame+ p2n.model -DEV=xlh
-Q=/cgm2.1/USPTO.spool.h/US09196161/runat.28062005.090806.20794/app.query.fasta_1.263
-DB=EST -OPMT=factap -SUFFIX=ret -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdd -LIST=45
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTPMT=ptc -NORR=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USBR=US09196161.QCGN.1.1.3437.0/runat.28062005.090806.20794 -NCPU=6 -ICPU=3
-NO_MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPELCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
EST:.*
1: gb_est1.*
2: gb_est2.*
3: gb_hic.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gsa1.*
9: gb_gsa2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	194	34.8	523	5	B0134970 INT1_2_D
2	194	34.8	540	5	B0134879 INT1_1_C
3	194	34.8	560	5	B0135128 INT1_3_F
4	194	34.8	622	5	B0134798 INT1_4_B
5	194	34.8	630	5	B0134905 INT1_1_F
6	194	34.8	631	5	B0134827 INT1_4_B
7	194	34.8	687	5	B0135168 INT1_4_B
8	181.5	32.5	514	5	B0134761 INT1_3_F
9	180.5	32.3	661	5	B0135189 INT1_4_D

10	175	31.4	592	5	B0134985	B0134985	INT1_2_G
C 11	144.5	25.9	419	5	B0135036	B0135036	INT1_2_D
C 12	144	25.8	675	5	B0135196	B0135196	INT1_1_B
C 13	140.5	25.2	502	5	B0134889	B0134889	INT1_1_D
C 14	140.5	25.2	590	5	B0135179	B0135179	INT1_4_C
C 15	140.5	25.2	602	5	B0135164	B0135164	INT1_4_B
C 16	140.5	25.2	607	5	B0134912	B0134912	INT1_1_F
C 17	140.5	25.2	658	5	B0135057	B0135057	INT1_2_G
C 18	139.5	25.0	538	5	B0134810	B0134810	INT1_4_C
C 19	139.5	25.0	559	5	B0134821	B0134821	INT1_4_D
C 20	136.5	24.5	445	5	B0134871	B0134871	INT1_1_B
C 21	133	23.8	150	5	B0135114	B0135114	INT1_3_F
C 22	132	23.7	210	5	B0134900	B0134900	INT1_1_E
C 23	89	15.9	711	6	CD873037	CD873037	AZ02_12D
C 24	88.5	15.9	565	1	A1516614	A1516614	LD42538.5
C 25	88.5	15.9	563	4	B1481638	B1481638	RB64226.5
C 26	88.5	15.9	639	1	A1515041	A1515041	LD46714.5
C 27	88.5	15.9	694	6	CD870573	CD870573	AZ02_114N
C 28	88.5	15.9	735	1	AA952214	AA952214	LD29313.5
C 29	88.5	15.9	876	8	B2399503	B2399503	EINCA214T
C 30	88	15.8	877	8	CC376965	CC376965	PURDU65TB
C 31	87.5	15.7	478	5	BQ810430	BQ810430	832013B04
C 32	87.5	15.7	569	2	AW070824	AW070824	1030017D0
C 33	86.5	15.5	524	5	BQ811391	BQ811391	1030002E0
C 34	86.5	15.5	531	5	BQ822580	BQ822580	1030101H0
C 35	86.5	15.5	788	8	B2385909	B2385909	EINBB85TF
C 36	86.5	15.5	919	1	AL522459	AL522459	Mus muscu
C 37	86.5	15.5	3140	3	AK086911	AK086911	AK086911
C 38	85.5	15.3	516	5	BX37323	BX37323	AL559722
C 39	85.5	15.3	1010	1	AL559722	AL559722	AL559722
C 40	85.5	15.3	1072	5	BX36097	BX36097	BX36097
C 41	85	15.2	558	2	BE441419	BE441419	925005F08
C 42	84.5	15.1	455	1	AA619168	AA619168	VO73B04.X
C 43	84.5	15.1	459	7	CN281628	CN281628	170005322
C 44	84.5	15.1	481	2	AM676151	AM676151	832007B01
C 45	84.5	15.1	602	7	CF557698	CF557698	1115030G0

ALIGNMENTS

RESULT 1
B0134970
LOCUS B0134970 523 bp mRNA linear EST 22-APR-2002
DEFINITION INT1_2.D10.b1.A006.G5.trophont cDNA (INT1) Ichthyophthirius
MULTIFILIS cDNA, mRNA sequence.
ACCESSION B0134970
VERSION B0134970.1 GI:20261069
KEYWORDS EST.

SOURCE
ORGANISM Ichthyophthirius multifiliis
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Ophryoglenina; Ichthyophthirius.

REFERENCE
AUTHORS Clark,T., Cordonnier-Pratt,M.-M., Sudan,M., Wentzel,V., Gingle,A.,
Dickerson,H., Lin,T.-L. and Pratt,L.H.
An EST database for Ichthyophthirius multifiliis (G5 isolate)
Unpublished (2002)
CONTACT: Cordonnier-Pratt MM

TITLE
JOURNAL
COMMENT Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmp@pratt.uga.edu

Sequences have been trimmed to exclude polyA, vector, and regions
below paired quality 16. The threshold for highest quality sequence
is 20.
Seq primer: JEN REV
High quality sequence stop: 508
POLYA=No.

FEATURES
source
1..523
/organism="Ichthyophthirius multifiliis"

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 30, 2005, 03:54:07 ; Search time 595 Seconds
(without alignments)
67.861 Million cell updates/sec

Title: US-09-196-161d-1

Sequence: 1 GAAGCAGANGOPFAANNAR.....PGCAPGVVFAAGAAAGV 105

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the local score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	558	100.0	442	17	US-10-878-694-5
2	221	39.6	468	17	US-10-878-694-5
3	87.5	15.7	3265	14	US-10-184-644-257
4	87.5	15.7	3265	14	US-10-184-644-257
5	87.5	15.7	3265	14	US-10-063-685-69
6	85.5	15.3	914	9	US-09-975-143-47
7	85.5	15.3	1076	14	US-10-028-072-219
8	85.5	15.3	1076	14	US-10-140-808-219
9	85.5	15.3	1076	14	US-10-121-049-219
10	85.5	15.3	1076	14	US-10-123-904-219
11	85.5	15.3	1076	14	US-10-140-470-219

12	85.5	15.3	1076	14	US-10-175-746-219	Sequence 219, App
13	85.5	15.3	1076	14	US-10-176-918-219	Sequence 219, App
14	85.5	15.3	1076	14	US-10-176-921-219	Sequence 219, App
15	85.5	15.3	1076	14	US-10-137-865-219	Sequence 219, App
16	85.5	15.3	1076	14	US-10-140-474-219	Sequence 219, App
17	85.5	15.3	1076	14	US-10-142-431-219	Sequence 219, App
18	85.5	15.3	1076	14	US-10-143-114-219	Sequence 219, App
19	85.5	15.3	1076	14	US-10-142-419-219	Sequence 219, App
20	85.5	15.3	1076	14	US-10-123-263-219	Sequence 219, App
21	85.5	15.3	1076	14	US-10-142-423-219	Sequence 219, App
22	85.5	15.3	1076	14	US-10-121-050-219	Sequence 219, App
23	85.5	15.3	1076	14	US-10-141-755-219	Sequence 219, App
24	85.5	15.3	1076	14	US-10-143-032-219	Sequence 219, App
25	85.5	15.3	1076	14	US-10-123-108-219	Sequence 219, App
26	85.5	15.3	1076	14	US-10-123-226-219	Sequence 219, App
27	85.5	15.3	1076	14	US-10-123-261-219	Sequence 219, App
28	85.5	15.3	1076	14	US-10-140-928-219	Sequence 219, App
29	85.5	15.3	1076	14	US-10-140-928-219	Sequence 219, App
30	85.5	15.3	1076	14	US-10-121-045-219	Sequence 219, App
31	85.5	15.3	1076	14	US-10-123-292-219	Sequence 219, App
32	85.5	15.3	1076	14	US-10-123-903-219	Sequence 219, App
33	85.5	15.3	1076	14	US-10-124-819-219	Sequence 219, App
34	85.5	15.3	1076	14	US-10-124-822-219	Sequence 219, App
35	85.5	15.3	1076	14	US-10-140-925-219	Sequence 219, App
36	85.5	15.3	1076	14	US-10-160-498-219	Sequence 219, App
37	85.5	15.3	1076	14	US-10-124-824-219	Sequence 219, App
38	85.5	15.3	1076	14	US-10-127-825A-219	Sequence 219, App
39	85.5	15.3	1076	14	US-10-127-829A-219	Sequence 219, App
40	85.5	15.3	1076	14	US-10-127-835A-219	Sequence 219, App
41	85.5	15.3	1076	14	US-10-127-839A-219	Sequence 219, App
42	85.5	15.3	1076	14	US-10-127-901A-219	Sequence 219, App
43	85.5	15.3	1076	14	US-10-128-633A-219	Sequence 219, App
44	85.5	15.3	1076	14	US-10-131-813A-219	Sequence 219, App
45	85.5	15.3	1076	14	US-10-131-818A-219	Sequence 219, App

ALIGNMENTS

RESULT 1
US-10-878-694-5
Sequence 5, Application US/10878694
Publication No. US20050106164A1
GENERAL INFORMATION:
APPLICANT: GABRTIG, Jacek
APPLICANT: DICKERSON Jr., Harry W.
APPLICANT: CLARK, Theodore G.
APPLICANT: THE UNIVERSITY OF GEORGIA RESEARCH FOUNDATION, INC
TITLE OF INVENTION: RECOMBINANT EXPRESSION OF HETEROLOGOUS NUCLEIC ACIDS IN
FILE REFERENCE: 235,00100101
CURRENT APPLICATION NUMBER: US/10/878,694
CURRENT FILING DATE: 2004-06-28
PRIOR APPLICATION NUMBER: US/09/498,612
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/118,634
PRIOR FILING DATE: 1999-02-04
PRIOR APPLICATION NUMBER: 60/122,372
PRIOR FILING DATE: 1999-03-02
PRIOR APPLICATION NUMBER: 60/124,905
PRIOR FILING DATE: 1999-03-17
PRIOR APPLICATION NUMBER: 60/131,121
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: PCT/US00/02966
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.10
SEQ ID NO 5
LENGTH: 442
TYPE: PRT
ORGANISM: Ichthyophthirius multifiliis
US-10-878-694-5

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OM protein - protein search, using sw model

Run on: June 30, 2005, 02:04:50 ; Search time 86 Seconds
(without alignments)
472.207 Million cell updates/sec

Title: US-09-196-161D-1

Perfect score: 558
Sequence: 1 GAAQGEAMGNQPFANNAAR.....PQGAFGVYFAAGAAAGV 105

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp19808:*
2: geneseqp19808:*
3: geneseqp20008:*
4: geneseqp20018:*
5: geneseqp20028:*
6: geneseqp20038:*
7: geneseqp20038:*
8: geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	558	100.0	409	3	AAB25889
2	558	100.0	442	3	AAV97176
3	558	100.0	442	3	AAB25859
4	297	53.2	89	3	AAB25862
5	261	46.8	83	3	AAB25861
6	258	46.2	89	3	AAB25863
7	221	39.6	468	3	AAV97177
8	221	39.6	468	3	AAB25882
9	221	39.6	468	3	AAB25860
10	119	21.3	76	3	AAB25885
11	139	24.9	69	3	AAB25864
12	102	18.3	72	3	AAB25888
13	91	16.3	1755	8	ADP31446
14	89	15.9	72	3	AAB25865
15	86	15.4	1464	8	ADP31437
16	85.5	15.3	1076	6	ABU6845
17	85.5	15.3	1076	6	ABU6845
18	84.5	15.1	1450	8	ADDO1059
19	84.5	15.1	1737	8	ADDO1057
20	84.5	15.1	1774	8	ABG59800
21	84.5	15.1	2778	7	ADCS1660
22	84.5	15.1	2789	7	ADG75733
23	84.5	15.1	2854	5	ADH48732
24	84	15.1	613	2	AAW73009
25	84	15.1	621	2	AAW73013

26	83.5	15.0	70	3	AAB25887	AAB25887 55KD I-an
27	83.5	15.0	739	6	AAO16358	AAO16358 Human tra
28	83	14.9	13	3	AAB25898	AAB25898 Ichthyoph
29	83	14.9	70	3	AAB25884	AAB25884 55KD I-an
30	83	14.9	1190	6	ADA74091	ADA74091 Equine Ia
31	83	14.9	1849	8	ADP30752	ADP30752 Human sec
32	82	14.7	472	8	ADP31222	ADP31222 Human sec
33	82	14.7	750	8	ADP31131	ADP31131 Human sec
34	81.5	14.6	525	8	ADP31227	ADP31227 Human sec
35	80.5	14.4	261	6	ADU21604	ADU21604 Protein e
36	80.5	14.4	1587	8	ADP30579	ADP30579 Human sec
37	80	14.3	320	8	ADP31607	ADP31607 Human sec
38	80	14.3	320	8	ADP31649	ADP31649 Human sec
39	79.5	14.2	531	8	ADP31696	ADP31696 Human sec
40	79	14.2	337	8	ADP31387	ADP31387 Human sec
41	79	14.2	5397	8	ADP31068	ADP31068 Human sec
42	78.5	14.1	605	8	ADL12887	ADL12887 Human ste
43	78	14.0	348	8	ADP30985	ADP30985 Human sec
44	78	14.0	2468	8	ADP30947	ADP30947 Human sec
45	78	14.0	3635	5	ABB81589	ABB81589 Mouse lam

ALIGNMENTS

RESULT 1
AAB25889 standard; protein; 409 AA.
ID AAB25889
XX AAB25889;
AC
XX
DT 18-DEC-2000 (first entry)
XX
DE IAG48 (GI) surface protein amino acid sequence.
XX
KW Immobilisation antigen; i-antigen; ichthyophthiriasis; vaccine;
KM white spot disease; freshwater fish; immune response; infection control.
XX
XX Ichthyophthirius multifiliis.
XX OS
XX WO200046373-A1.
XX
PD 10-AUG-2000.
XX
XX
XX 04-FEB-2000; 2000MO-US002962.
XX
XX 04-FEB-1999; 99US-0118634P.
XX
XX 02-MAR-1999; 99US-0122372P.
XX
XX 17-MAR-1999; 99US-0124305P.
XX
XX 27-APR-1999; 99US-0131121P.
XX
XX (UYGE-) UNIV GEORGIA RES FOUND INC.
XX (COOR) CORNELL RES FOUND INC.
XX (CLAR) CLARK T G.
XX (DICK) DICKERSON H W.
XX (LINT) LINT T.
XX
XX Clark TG, Dickerson HW, Lin T;
XX WPI; 2000-506071/45.
XX
XX Novel i-antigen polypeptides and polynucleotides from Ichthyophthirius
XX multifiliis, useful for prophylaxis and treatment of Ichthyophthirius
XX infection in fish.
XX
XX
XX Disclosure; Fig 8; 144pp; English.
XX
XX This invention relates to novel i-antigen polypeptide sequences. I-
XX antigens or immobilisation antigens are common to a variety of
XX hymenostomatid ciliates and their expression varies in response to
XX environmental stimuli. This invention relates to i-antigen in
XX Ichthyophthirius multifiliis, a protozoan which is an obligate parasite
XX of freshwater fish causing Ichthyophthiriasis or white spot disease. The

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OM protein - protein search, using sw model

Run on: June 30, 2005, 02:08:15 ; Search time 93 Seconds
(without alignments)
578.154 Million cell updates/sec

Title: US-09-196-161d-1
Perfect score: 558
Sequence: 1 GAAQGEANGNPAPANNAAAR.....PQGEAPGVPPAAGAAAGV 105

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	558	100.0	395	2	Q27208
2	558	100.0	442	2	Q27208
3	222	39.8	460	2	Q962N5
4	221	39.6	468	2	Q962N5
5	93.5	16.8	371	2	Q962N5
6	93	16.7	548	2	Q962N5
7	93	16.7	677	2	Q962N5
8	88.5	15.9	305	2	Q962N5
9	88.5	15.9	316	2	Q962N5
10	87	15.6	724	2	Q962N5
11	85.5	15.3	518	2	Q962N5
12	85	15.2	316	2	Q962N5
13	85	15.2	536	2	Q962N5
14	85	15.2	632	2	Q962N5
15	85	15.2	632	2	Q962N5
16	84.5	15.1	245	2	Q962N5
17	84.5	15.1	2330	1	EFLA_MOUSE
18	84.5	15.1	2386	1	EFLA_MOUSE
19	83	14.9	1190	2	Q962N5
20	81.5	14.6	814	2	Q962N5
21	81	14.5	130	2	Q962N5
22	81	14.5	1827	2	Q962N5
23	80.5	14.4	560	2	Q962N5
24	80	14.3	338	2	Q962N5
25	79.5	14.2	1019	2	Q962N5
26	79.5	14.2	1019	2	Q962N5
27	79	14.2	155	2	Q962N5
28	79	14.2	600	2	Q962N5
29	79	14.2	3333	1	LMAS_MOUSE
30	78.5	14.1	239	2	Q962N5
31	78.5	14.1	821	2	Q962N5

32	78	14.0	596	2	Q07317
33	78	14.0	833	2	Q61288
34	78	14.0	3718	1	LMAS_MOUSE
35	77.5	13.9	484	2	Q951G2
36	77.5	13.9	569	2	Q70XT3
37	77.5	13.9	573	2	Q9HMOQ
38	77.5	13.9	1997	2	Q81RM7
39	77.5	13.9	3467	2	Q81218
40	77	13.8	166	2	Q9B1K0
41	77	13.8	424	1	ASP_ANCCA
42	77	13.8	424	2	Q9XZ41
43	77	13.8	776	2	Q70NG0
44	77	13.8	1372	2	P91526
45	77	13.8	1546	2	Q75445

ALIGNMENTS

RESULT 1	Q27208	PRELIMINARY;	PRT;	395 AA.
AC	Q27208			
DT	01-NOV-1996 (TREMBLrel. 01, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, last sequence update)			
DT	01-MAR-2004 (TREMBLrel. 26, last annotation update)			
DE	Immunoblotting antigen precursor (fragment).			
OS	Ichthyophthirius multifiliis (White spot) (Ich).			
OC	Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;			
OC	Ophryoglenina; Ichthyophthirius.			
OX	NCBI_TaxID=5932;			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Georgia;			
RX	MEDLINE=9230590; PubMed=1383510;			
RA	Clark T.G., McGraw R.A., Dickerson H.W.;			
RT	"Purification and partial characterization of immunoblotting antigens from Ichthyophthirius multifiliis".			
RT	J. Protozool. 39:457-463(1992).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Georgia;			
RA	Clark T.G.;			
RL	Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; M92907; AAC6158.1; -.			
DR	PIR; A46031; A46031.			
DR	GO; GO:0005489; F:electron transporter activity; IEA.			
DR	GO; GO:0005506; F:ion ion binding; IEA.			
DR	GO; GO:0006118; P:electron transport; IEA.			
DR	InterPro; IPR001450; 4Fe4S ferredoxin.			
DR	InterPro; IPR009030; Grow_Fac_recept.			
KW	PRINTS; PRO0353; 4FESFRDXIN.			
KW	Signal.			
FT	NON_TER			
FT	SIGNAL			
FT	CHAIN			
SO	SEQUENCE			
Query Match	395 AA; 39567 MW; 68DA2C790A4FD393 CRC64;			
Best Local Similarity	100.0%; Score 558; DB 2; Length 395;			
Matches	105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1 GAAQGEANGNPAPANNAAARICVPCQINRVSVNAGDLATATGCTGCTGALDDG 60			
DB	37 GAAQGEANGNPAPANNAAARICVPCQINRVSVNAGDLATATGCTGCTGALDDG 96			

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OM protein - protein search, using sw model

Run on: June 30, 2005, 03:41:16 ; Search time 25 Seconds
(without alignments)
404.110 Million cell updates/sec

Title: US-09-196-161d-1

Perfect score: 558

Sequence: 1 GAAQGEANGNQFPANNAAR.....PGSEAGVGFPAAGAAAGV 105

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 79: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	558	100.0	395	2 A46031	Immunoglobulin sur
2	93	16.7	677	2 C42125	Trophozoite cyste
3	84.5	15.1	1737	2 T00209	MEGF protein - hu
4	78	14.0	596	2 A45664	variant-specific s
5	78	14.0	3635	2 T10053	laminin alpha-5 ch
6	77.5	13.9	573	2 D83130	probable iron-sulf
7	77	13.8	1372	2 T25933	hypothetical prote
8	77	13.8	3712	2 S18253	laminin alpha-1 ch
9	75.5	13.5	713	2 A35502	major surface-labe
10	75	13.4	1193	2 A44018	laminin B2c chain
11	75	13.4	3084	1 MMSA	laminin alpha-1 ch
12	72.5	13.0	398	1 S24802	polyferredoxin 6x2
13	72.5	13.0	2225	2 T26063	hypothetical prote
14	72	12.9	109	2 S18323	thryoglobulin - bu
15	71	12.7	610	2 JCT530	vascular apoptosis
16	71	12.7	1713	2 A55347	adhesive ligand ep
17	70.5	12.6	289	2 T25682	hypothetical prote
18	70.5	12.6	1607	1 MMSB2	laminin gamma-1 ch
19	70	12.5	485	2 S36772	B-selectin - bovin
20	69.5	12.5	2824	2 T22759	hypothetical prote
21	69	12.4	610	2 JCT8056	halysae - Gloydin
22	69	12.4	1557	2 T25811	hypothetical prote
23	68.5	12.3	371	2 C97559	conserved hypotet
24	68.5	12.3	371	2 AH2779	protein P11C7.3 (l
25	68.5	12.3	425	2 C89753	ccog protein - Par
26	68.5	12.3	484	2 S77602	subtilisin-like pr
27	68.5	12.3	962	2 JCT571	subtilisin-like pr
28	68.5	12.3	969	1 A39490	subtilisin-like pr
29	68.5	12.3	975	2 JCT5570	subtilisin-like pr

30	68.5	12.3	1280	2 A39117	170K lectin precur
31	68.5	12.3	1695	2 T15881	hypothetical prote
32	68.5	12.3	2014	2 T21560	hypothetical prote
33	68	12.2	738	2 S40992	hypothetical prote
34	68	12.2	739	2 B88553	protein K04H4.2b l
35	67.5	12.1	496	2 F87423	ferredoxin, probab
36	67.5	12.1	932	2 I52527	PACSA4 - mouse (fr
37	67	12.0	294	2 T21668	hypothetical prote
38	67	12.0	314	2 I37383	PAS soluble protei
39	67	12.0	335	2 A40036	apoptosis-mediati
40	67	12.0	439	2 A36385	surface antigen se
41	67	12.0	510	2 AD1554	D-alanine-actylat
42	67	12.0	563	2 AB3417	electron-transfer
43	67	12.0	1639	1 MMRFB2	laminin gamma-1 ch
44	67	12.0	1827	2 T34288	hypothetical prote
45	67	12.0	3075	2 S14458	laminin alpha-1 ch

ALIGNMENTS

RESULT 1
A46031
Immunoglobulin surface I-antigen precursor - Ichthyophthirius multifiliis (fragment)
C/Species: Ichthyophthirius multifiliis
C/Date: 29-Sep-1999 #sequence_revision 29-Sep-1999 #text_change 09-Jul-2004
C/Accession: A46031
R/Clark, T.G.; McGraw, R.A.; Dickerson, H.W.
Proc. Natl. Acad. Sci. U.S.A. 89, 6363-6367, 1992
A/Title: Developmental expression of surface antigen genes in the parasitic ciliate Ichth
A/Reference number: A46031; MUID:92335298; PMID:1631132
A/Accession: A46031
A/Molecule type: mRNA; protein
A/Residues: 1-395 <CLAS>
A/Cross-references: UNIPROT:Q27208; GB:M92907; NID:93628568; PIDN:AC36158.1; PID:9362856
A/Note: the authors translated the codon UUG for residue 330 as Ile
A/Note: sequence extracted from NCBI backbone (NCBIN:108734, NCBIPI:108735); the sequence
C/Genetics:
A/Genetic code: SGC5
C/Keywords: glycoprotein; surface antigen
F/2-395/Product: Immunoglobulin surface I-antigen #status experimental <MAY>
F/156,191,245,281/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 100.0%; Score 558; DB 2; Length 395;
Best Local Similarity 100.0%; Pred. No. 1.5e-46;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAQGEANGNQFPANNAARGICVPCQINRVGSVTNAGLTLATOCSTQCPGTALDDG 60
DB 37 GAAQGEANGNQFPANNAARGICVPCQINRVGSVTNAGLTLATOCSTQCPGTALDDG 96
QY 61 VYDVDPBSAACCVCCKPNFYNGSGPGEAPGVQVFAAGAAAGV 105
DB 97 VYDVDPBSAACCVCCKPNFYNGSGPGEAPGVQVFAAGAAAGV 141

RESULT 2
C42125
Trophozoite cysteine-rich surface antigen 72 - Giardia lamblia (fragment)
N/Alternate names: CRP72
C/Species: Giardia lamblia
C/Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 09-Jul-2004
C/Accession: C42125
R/Adam, R.D.; Yang, Y.M.; Nash, T.E.
Mol. Cell. Biol. 12, 1194-1201, 1992
A/Title: The cysteine-rich protein gene family of Giardia lamblia: loss of the CRP170 ger
A/Reference number: A42125; MUID:92186850; PMID:1545800
A/Molecule type: DNA
A/Residues: 1-677 <ADA>
A/Cross-references: UNIPROT:Q7M3R4; GB:M83934; NID:9159123
A/Experimental source: trophozoites
A/Note: sequence extracted from NCBI backbone (NCBIN:88443, NCBIPI:88444); this ORF is not